

Figure 1 A.

BD fusion	AD fusion	-His growth	-Leu growth	β -gal activity	-Ade-Trp growth
MPK4	MKS1	+	+	+	+
MKS1	MPK4	+	+	+	+
MKS1	MPK3	-	-	-	+
MKS1	MPK5	-	-	-	+
MKS1	MPK6	-	-	-	+
MKS1	MPK17	-	-	-	+
MKS1	WRKY25	+	+	+	+
MKS1	WRKY33	+	+	+	+
MKS1	WRKY26	-	-	-	+
MKS1	WRKY29	-	-	-	+
MPK4	WRKY25	-	-	-	+
MPK4	WRKY33	-	-	-	+

Figure 1B (1)

1-----Pep22-----1

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1 MSSTSSSPPPPSK-----AKRRGCHGARPOPLIVSSAPAEASRPSKKPRVS-----GGG
1 MSSTSSSPPPPSK-----AKRRGCHGARPOPLIVSSAPAEASRPSKKPRVS-----GGG
1 MTMTVATMPSSDASSSPFKRPTATGGGILGPRRPEPLKVTSSSPSSSSSSSRSSSPAS-NKP-----PASTT
1 MTMTVAMPSSS-----SSRRGGLRGPRPEPLKVSSSSSRGSSPSSSASKG-----ASKK
1 -----SLOGPRPEPLILPPGSGTTSSSSSSSTPRPA-KRPRRVVSGGGGDVSRAPQSSA
1 -----MDPSEYFAGGNPSDQONQKRLQICGPRPEPLSVNKDSHKIKKPP-----KHPAPPP-NRDQPPPY
1 -----MDPSESFAGGNPSDQONQKRLQICGPRPEPLSVNKDSHKIKKPP-----KHPAPPPQ-HRDQAPLY
1 -----MDPSEHFAGGNPFDQOTPRQLOICGPRPEPLSVNKDSHKIKKPP-----RHPAPPPQHHRDQAPLY
1 -----OLOGPRPEPLRINKDSHKIKKPP-----LAPQPSHP-----HQP
1 -----MDNRSPSRGILGPRPEPLKVRGDSHKIKKPPPLAPP-----PQPQPPQTHQOEPSQSR
1 MEFPSSSTSPSPSSSGQHQQOPTTFRROLOGPRPEPLNVRMESHAIKKPSSGAAAA--AAQAQAHQLPAQAQARREQQQP
1 MDPPSSSG-----RPTTPRRROLOGPRPEPLNVRMESHAIKKES-----ASGAPPAPGQGRPRDHHHHHPQ
1 -----CGPRPEPLAVSKDSHKYRKPFVAPQROQHQQQPAAQLQQQQQHQQHQQQQQ
1 -----MDQSSSTLLINQ-----RKSSSSPTTIPPKOK-----RKSTT
1 -----MESSSSTFLTTSILDKKPSPVSRKSPKOK-----KKTTS
1 -----MVRNSMKAEDIDHLPHTFYGDYSKTLVPMNNS-----QIITK
1 -----MEITQYQSFH-EGSSSRVSMNNS-----QVISK
1 -----MEATIFEKRSSLSSIAVHKOS-----YSITK
1 -----MEIEATTVQKRS-LPTIAMHKOS-----RTLTK
1 -----MEQQLSSPSASQGGGRELQGRPEPLKVRGESHKIKKOE-----PVQ
1 -----MIPTRCNEINGSRPSLSKLAGESEHTIKTSCKSKP-----RPH
1 -----MPSRSSMASPLLORPHDLLGPRPEPLKVSSTGTITTTGTADLQLOVVN-----RR
1 -----MDROQQSSRGNATATRGGGSSGSGGGGGVG-----KAA
1 -----MAAASFDAADVTRRGCTGRALGVHAASHKIKKPPGAG-----HGO
1 -----MSKAAKN-----
1 -----NFKDVIQRLTKPFDNKQPAKAGEVSPAER-----LASI
r      i gprp l v dsh ikk      tk
          DOMAIN 1

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1C3 DELETION

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51 GDTGPVIVYEL-PRVVHVEQEEFMVVKLTGG-----KQOPAAASTLTTL
51 GDTGPVIVYELTPRVVHVEQEEFMVVKLTGG-----KQOPAAASTLTTL
56 AKRPVIVYEHPTPVVHASPOEFMTVQRLTG-----KRPRAPTSS--
50 SAAAPVIVYEHPTKVVHARPOEFMTVQRLTG-----KPPAAPVMMMPA
53 AAGPVLIVYEHPTKVVHARADEPKALVQSLTG-----RGGCEAVER--
61 IPREPVLIVYAVSPKVVHATASEFMVQRLTGISSGV-----FLESGGGDVSPAAR
62 AAREPVLIVYAVSPKVVHTTASDFMNVQRLTGISSAV-----FLESNGGDVSPAAR
63 PPREPVLIVYAVSPKVVHTTTSDFMNVQRLTGISSEV-----FLESNDGDVSPAAR
35 PPROPLIIVYTVSPKVIHTTSPDFMNLVQRLTGSSSSS-----SAEVVMSNNNN--
56 PPPGPVLIVYTVSPRIIHTHPNFTLVQRLTGKTSTS-----TTSSSYSSSTSA PKD
79 PPRAPVLIIYDASPKVIHAKPNEFMALVQRLTGP GSGPPAPPHQGEAQADYPMDEAAAQOFFPPELLLSPSAAMSPAAR
61 PGRAPVLIIYDASPKVIHAKPSEFMALVQRLTGPQAQAQHERHVADDDATAN--GGGVLGQAFLLPELLLSPSAAMSPAAR
52 QGRAPVLIIYDASPKVIHTKPGDFMALVQRLTGP GSTSQAQFDAAAAAAGPS-----HPAAMEFEPREFLLSPTAALSPAAR
33 THRPKIRVYIISNPMRVETCPSEKRELVOELTG-----QDAADLPEEPT
36 TNKPKIRVYIISNPMRVQTCASEKRELVOELTG-----QDAVDLOHEPI
41 IKPKIRLIHIFAPELITDVKNERLVLQSLTG-----KPE--LTKTGS
29 IKPKIRLIHIFAPEVITDVKNERSLVQSLTG-----KPAPGEAKTGK
28 SKPKIRLIHIFAPELIKTDVANERELVQSLTG-----KPDQORTSKAK
29 SKPKIRLIHIFAPELIKTDVANERETVQNLTG-----KQDHHHEDLPH
44 QLRAPVLIIYTMSPKVVHANADFMVQRLTG-----APPTAPPQOPH
40 GRASEPVLIIYAHSPKVIHTRAEDFMALVQRLTG-----LDEIIRNTSESS
50 RRRAPVLIIYVESPRVHAHPAEKSVQRLTG-----TAPALELPL
35 GGRPKIVYIISNPMRVKTSAAGRALVQELTG-----RNDPSKYSFR
43 QRRAPVLIIYVSPKVVIHVDAHEFMVQRLTG-----PEAGGRKSRPS
8 -MTVPKIRIVENTQYLETDASSKSVQRLTG-----NSTVEMVAAPP
35 QRTSPKKKQRFVNRDEHMMQMLDEGVQMGQVPG-----ILLSSTLPP
kr pviiv SPkviht efm lVQrLTG      rpaaevSP pr
          DOMAIN 2

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Figure 1B (2)

!C2 DELETION

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96 PAADQVAGGDHAAAAAATDPTVLTG--QORQAPAPAPAIIDGHPAAPPSPADA-----FILSPSSFFLSPTTMBALQ
97 PAADQVAGGDHAAAAAARADPLVLTIGQORQAPAPAPAIIDGHPAAPPSPADA-----FILSPSSFFLSPTTMBALQ
108 --LPSGTVSPAATAEAGGCDPILLITIGORQ--AAAPAPPTTITLLPSSAMAAAG-----MLSPG--FIESPSTMOAIQ
94 YDAPAMVEQCAAAACAGGDPILLITIGORQ--AASAPAPPPAVPSP--LMAAG-----MLSPG--FIESPNTMQSIQ
95 -----PPASSQOTAACOLLVLTIGHHQH--VPPPPP--LPSP--GCAAG-----FILSPGSETESPATMOAIQ
113 LAATENASPRGCKE-----PAARDETVEINTAMEEAAEFGGYAPGILSPSPAI-----LPTASTGIESPMYHOQGM
114 LAATENASPRGCKEPV-----MAAKDETVEITAMEEAAEFSGYAPGILSPSPAM-----LPTASAGIESOMTHOQGG
115 LAATENASPRGCKE-----PVESSTAMEEAAEFGCYVPGILSPSPAM-----LPTVPAGIESPMFHLGGL
83 -----TTHVDFENNGCGGVSPAPARYATHEKAM-----SPMCKKEMILLESVNNIIS
108 ASTMVDTSGLISPAARFVTEKANTSNELCTFVGGEETMDQYYHYHHHHHHQOE-----QOHONOCFERPSFHHAGT
159 LATIERSVRPMP-----EPABEYVDITNGGCGCGVDDCGIAAILGSIRPGILSP--LPSSLPPAAVPCOESPLPFASC
139 LATIERSVRPVP-----APAPAPDYAADG-----HPRGGARPREAPR--HPVPAAVLAAAGRRVGPVLAAM
128 LATIERSVRPLPPHAPAAVEPYFGATNDDCFILPGSADMDSLAALGPPACRPGILSPAALPPAASGLSPMPFDSC
76 TF-----TAVDLHRPCESENNLEP-----LDGEVRCEIYSPDEEVFNAP--QM-----SAGLSGFFSSG
79 YS-----PSSDDHNLSPPAENLAPRVLHQEPFGERDSDCYEPLNAEDMFLPDQM-----SAGFSGFFSNG
82 KK-----KITNTNFPAPPCLQODSGOEHTAELDNRIIG--SHYVKEEWGS-----SSNTNTYEDFDGLIDLD
72 KR-----AKSRITTPQEPVCDHQPVRNLSGFTGLLANGGNHGVKEEWGSGDQS-----TSNTNTYEDLEGLIQDV
71 PR--RDMERLHRQVQDMINTEKLREPEHCDQEFCLNAEETSMTWNGNNGAGESS-----GGFLNGLGDFEGFIQEL
72 QKGLKRNPSRRSHDHHEVDMNKSNGFCINSDEEEECMVSMTWNGN--GDESS-----GGFLNGLGDLGDFIQEL
88 HPTLLAQMPQPSFFPHLQQODAWPQQCHSPAALIEQAAARSSGADLPPLPSILSP--VPGTVLPAIPASEFSPPSLISPV
85 SSVVTEEVNVGDDNTAAPPFSDRTORQKLTDMPLFTPSSTMLFGSPTQLMYMSP-----NRDSEPLVFKSE-
91 KFFHFHFHFPSSVGAASRALLETSSSTSSGVMSVVTVDITCGGGSVPQOLPNHH-----MLVSSDPCDLPPLPSLIRVIL
78 ASADDDDDGGCGGGGGGELAAASDGAGEFGPCAASPDTGAAAASDAADALVAAG-----HPAATDEDEGGGGGG
88 TSGVGGGAGEAEPSEGAENKTRAAPPVRVKARALNRPVSVTTRRQQAADASP-----PSGLMLFQDLSPERGA
53 PTAAANYVREGYNWDDQSSRALISETESIARKPSPLGRGMSFNDFDNTEKELP-----PVDDLRLRYADEYRSNY
80 ISSENFSLSLSPSTPLYTFSPETFSPTSYIFSPEKNMLVPSNIDRKGTIPTMQS-----EVYPQNMHQRILSKFLGG
aam h aat a aa pl tltq a am aa lt la g m aal lpsa sgifSP tm a m

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!C1 DELETION

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168 EEEAARRVVEATSTGLGVQSGKSSQDTVNLHADANAAAAAALAAHSSRGPRSSSTOPP----- a
170 ELAALF----- b
177 ELNPLF----- c
162 ELSPLF----- d
152 EIIS----- e
179 FS-----PAIPLGLFSPAGFMSFPRSPGFT-----SLVASPTFADFFSHIWDQD----- f
182 MF-----SPG--LFSPAGLMSFG--FA-----SLVASPTFADLFSHIWG----- g
175 FS-----PALPPGLFSPAGLMSPGYAS-----LASPNFADFFSHIWDP----- h
129 DV-----E----- i
180 LSPGPNLSLPSVSPDFSTIGPTDPQGFSSFFNDFNSILQSSPSKIQSPSSMDLFNNFFDS----- j
231 ISWLNELSPIIRAASAGAASSSGGGGSGGNTSNGGAARPPPSYYADPFVPSPRHLLATPTVPSPATCAELFSNLPDL k
199 RPQQRQLAQRAQPHPPGVSVGORSAPLAHAGPTGGSROP----- l
208 LSWLSELSPFLPSAGTRAAAGLLDQAPFAPSRSLLSTPTMPS--PATFSVLEFFSSPNFPDL----- m
129 -----FYNVNALGSIGSL----- n
139 -----FYNVNDFGSIDSM----- o
142 -----EDDNIFSRWFDLQQO----- p
138 GEDYFSSFFMRSSSSSQVEGFIFNNNNNNNNNNNNNNNNNNNTNFDTKAHNSS----- q
140 G-----EFPYLPLSSIDASASSNSS----- r
141 G-----EFPYLPFTIDPAVASSSHLGNVFAEPHHYA----- s
166 PFLGATTSSAAPSTSPSPMGGSAYYWDLFNMQQQYHHQN----- t
----- u
165 SSNTTAVVSSSTNTSKNYE----- v
148 GYYDDDDDDIFRSQLLDTYSVFSPTLLYDHPHKS----- w
159 LKGEHLPLVSPAULHHVGDHFLSPAGAAAALGSPSPSEVDDIFGTLSSQQO----- x
125 ----- y
156 AKFP----- z

```

a: OsBAC15955	b: Os8355.t00567	c: ZmCC661221	d: Os8360.t05160	e: ZmBM340911
f: MKS1 At3g18690	f: BoBH544707	g: BoBOHBT92TR + BOGQI24TF	h: GmBE020960	
i: At1g21326	j: OsCAD40925	k: ZmCC613160	l: ZmCC635639	m: At2g41180
n: AtAL390921	o: AtAL138658	p: At2g44340	q: AtT46022	r: At2g42140
s: OsAP004654	t: At1g68450	u: ZmCC442903	v: OsAP003260	w: ZmCC700850
x: Ntacre169	z: MtAC143340.1			

Figure 2.

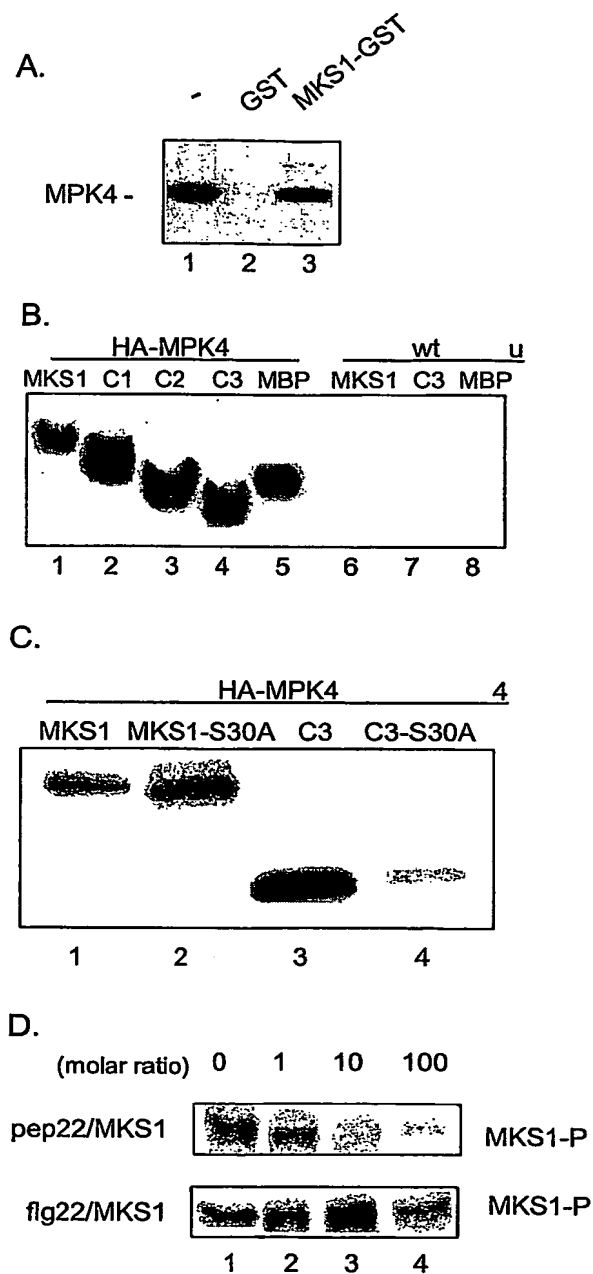


Figure 3.

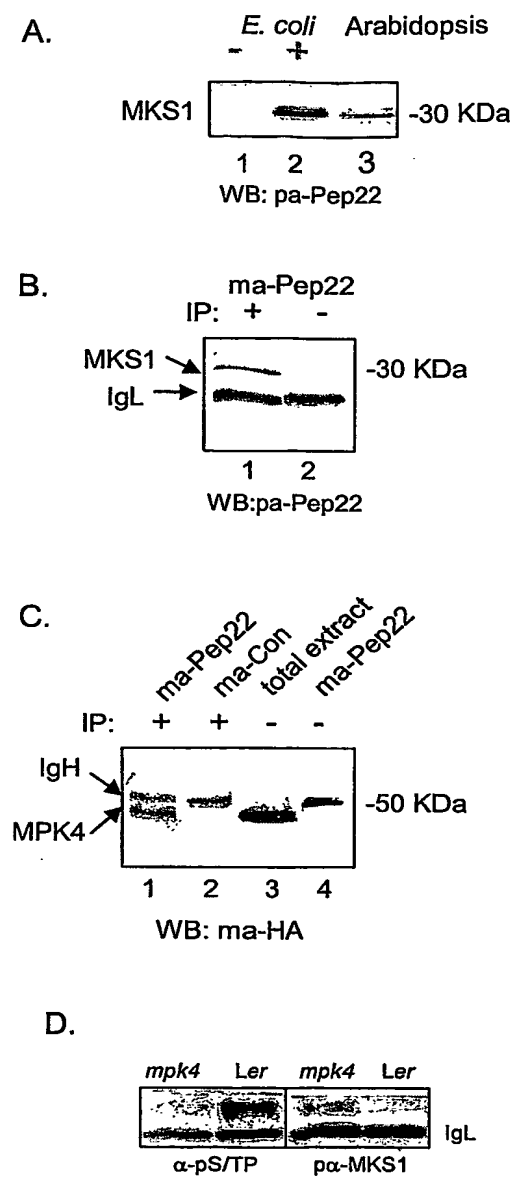
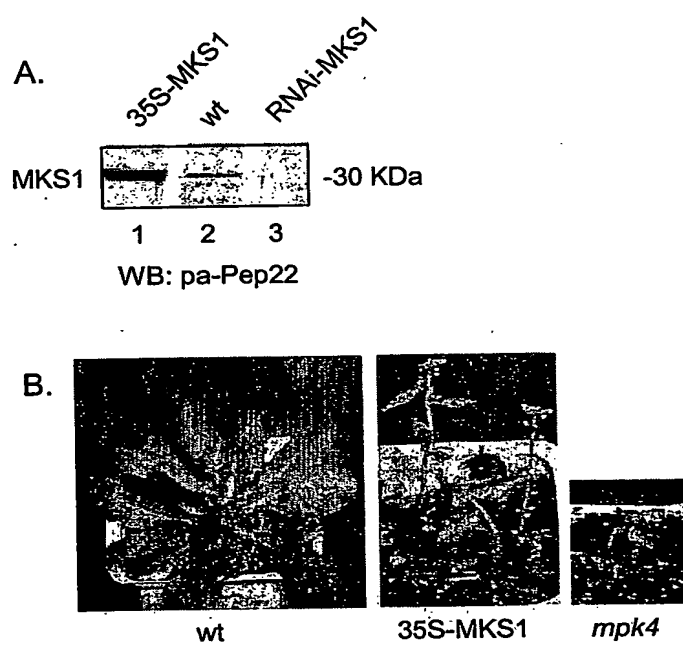
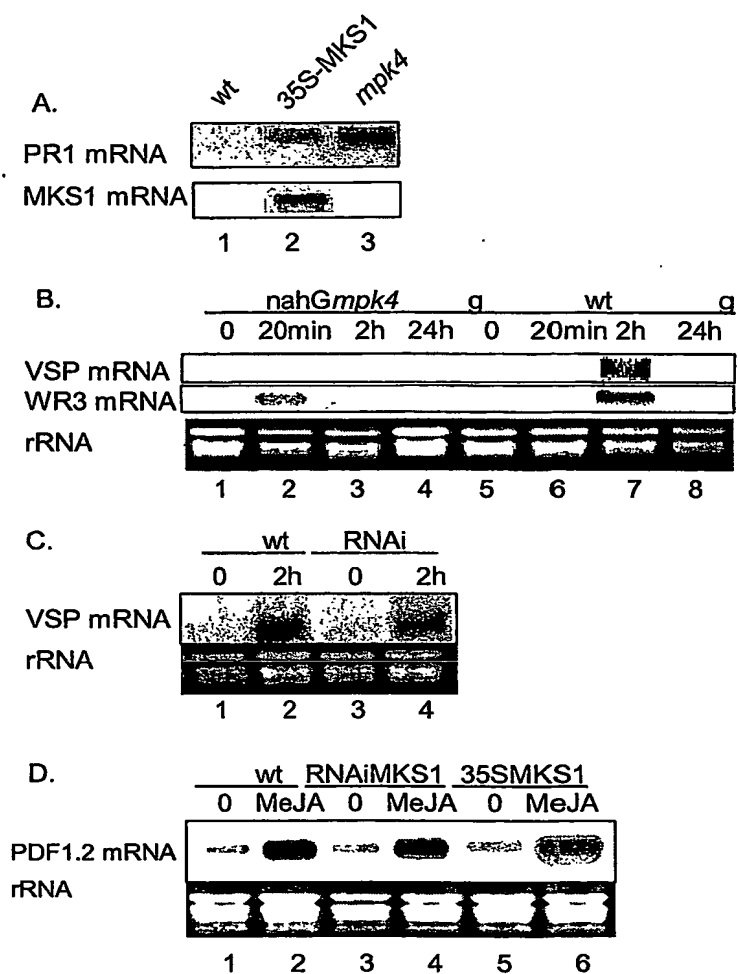


Figure 4.



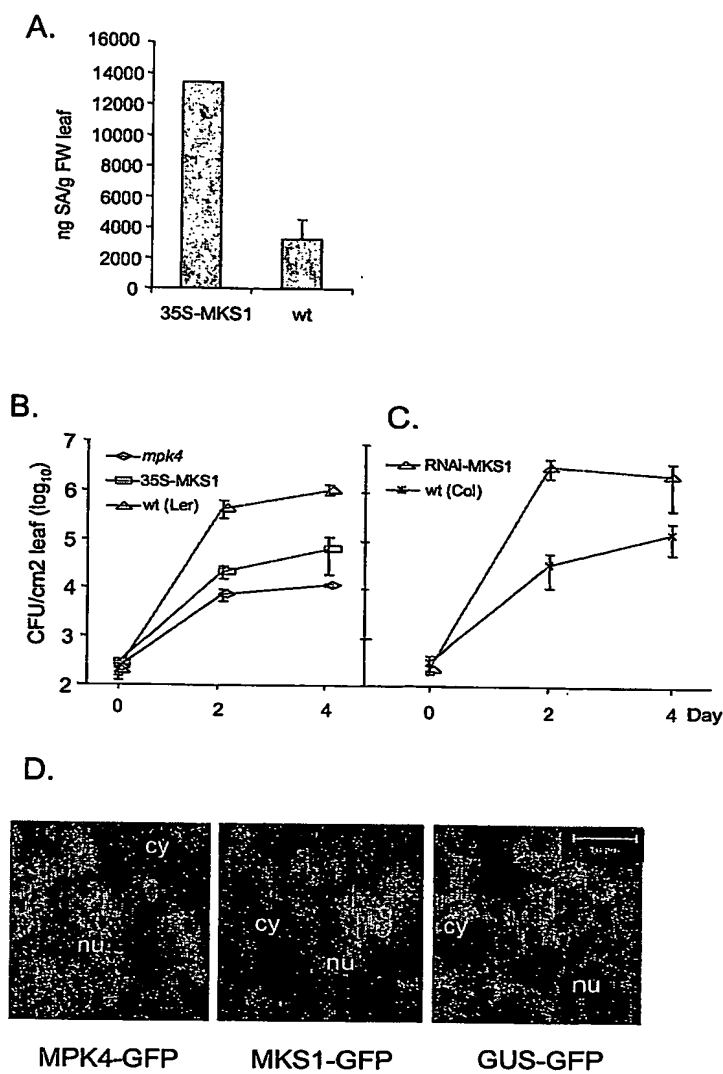
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Figure 5.



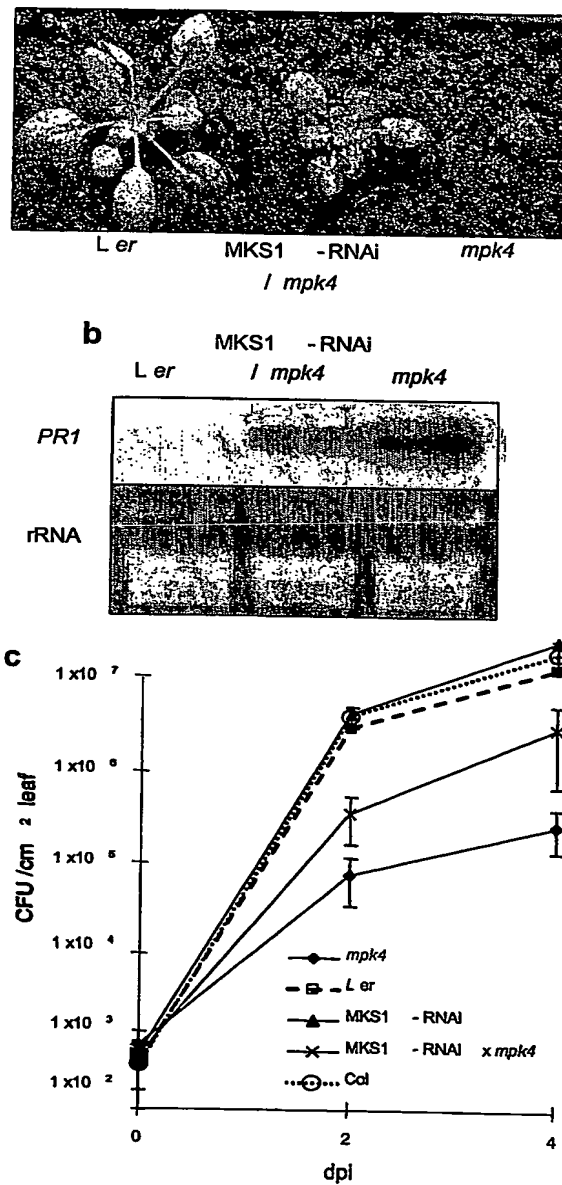
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Figure 6.



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Figure 7



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Figure 8.

